SEQUENCE LISTING

<110> NIIGATA TLO CORPORATION

<120> Vector for gene therapy and method for quantifying target protein in mammal or cultured cell to which the vector for gene therapy was administered

<130> 03PF275-PCT

<150> JP 2003-3967
<151> 2003-01-10

<160> 24

<210> 1
<211> 11
<212> PRT
<213> Artificial Sequence
<220>
<223> oligopeptide encoding C19-29 region of glucagon of human, mouse or rat

<400> 1

Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
1   5   10

<210> 2
<211> 1471
<212> DNA
<213> Artificial Sequence
<220>
<221> CDS
<222> (13)..(1461)
<223> DNA insert encoding rat IFN-r receptor, rat IgG Fc region and glucagon C19-29 region

<400> 2

```
gaattcattt aa atg att ctg ctg gtg gtc ctg atg ctg tct gcg gag atc        51
               Met Ile Leu Leu Val Val Leu Met Leu Ser Ala Glu Ile
                1               5                   10


ggg agt gga gct ttg atg agc acc gag gat cct aag ccg ccc tcg gtg           99
Gly Ser Gly Ala Leu Met Ser Thr Glu Asp Pro Lys Pro Pro Ser Val
         15                  20                  25


cct gcg cca aca aat gtt cta att acg tcc tat gac ttg aac cct gtc          147
Pro Ala Pro Thr Asn Val Leu Ile Thr Ser Tyr Asp Leu Asn Pro Val
30                  35                  40                  45


gta cat tgg aag cac cag aac gtg tcg cag gct gcc gtc ttc act gta         195
Val His Trp Lys His Gln Asn Val Ser Gln Ala Ala Val Phe Thr Val
                50                  55                  60


cag gta aag atg tat cca gaa tac tgg act gat gcc tgc acc aac att         243
Gln Val Lys Met Tyr Pro Glu Tyr Trp Thr Asp Ala Cys Thr Asn Ile
                65                  70                  75


gcc cat cat tat tgt aat atc tac aaa cac att tcc tat cct gac tca         291
Ala His His Tyr Cys Asn Ile Tyr Lys His Ile Ser Tyr Pro Asp Ser
             80                  85                  90


tct gcc tgg gcc aga gtt aag gcc aag gtt gga caa aga gaa tct gcc         339
Ser Ala Trp Ala Arg Val Lys Ala Lys Val Gly Gln Arg Glu Ser Ala
     95                  100                 105


tat gcg cag tca gaa gag ttt att atg tgc cga aag ggg aag gtt gga         387
Tyr Ala Gln Ser Glu Glu Phe Ile Met Cys Arg Lys Gly Lys Val Gly
110                 115                 120                 125


ccg cct ggc ctg gac atc gga agg aag gaa gat cag ctg att gtc cac         435
Pro Pro Gly Leu Asp Ile Gly Arg Lys Glu Asp Gln Leu Ile Val His
```

                    130   135   140

ata ttt cac cct aag gtc aat gtg agt cag gaa acc atg ttt ggt gac   483
Ile Phe His Pro Lys Val Asn Val Ser Gln Glu Thr Met Phe Gly Asp
            145   150   155

gga aat acc tgt tac aca ttc gac tac act gtg ttt gtg aaa cat tac   531
Gly Asn Thr Cys Tyr Thr Phe Asp Tyr Thr Val Phe Val Lys His Tyr
            160   165   170

agg agt ggg gag atc cta cat aca gaa cat agc gtc cta aaa gaa gat   579
Arg Ser Gly Glu Ile Leu His Thr Glu His Ser Val Leu Lys Glu Asp
        175   180   185

tgt agc gaa act ctg tgt gag tta aac atc tca gtg tcc acg ctg aat   627
Cys Ser Glu Thr Leu Cys Glu Leu Asn Ile Ser Val Ser Thr Leu Asn
190   195   200   205

tcc aat tac tgt gtt tca gta gtt gga aag tcg tct ttc tgg caa gtt   675
Ser Asn Tyr Cys Val Ser Val Val Gly Lys Ser Ser Phe Trp Gln Val
            210   215   220

aat aca gaa aca tca aaa gac gcc tgt atc ccc ttt ctc cat gat gac   723
Asn Thr Glu Thr Ser Lys Asp Ala Cys Ile Pro Phe Leu His Asp Asp
            225   230   235

aga gaa gaa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc aag   771
Arg Glu Glu Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys Lys
            240   245   250

cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc ccc   819
Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe Pro
        255   260   265

cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc acg   867
Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr

		270				275				280				285			

tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc agc   915
Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe Ser
           290   295   300

tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca cca   963
Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro Pro
           305   310   315

gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc atc   1011
Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile
           320   325   330

ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc acc   1059
Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val Thr
           335   340   345

agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc gaa   1107
Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro Glu
350   355   360   365

ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag gaa   1155
Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys Glu
               370   375   380

gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc ttc   1203
Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly Phe
               385   390   395

tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca cag   1251
Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro Gln
           400   405   410

gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt tac   1299
Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser Tyr

415   420   425

ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag gga   1347
Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln Gly
430   435   440   445

aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac cat   1395
Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His
                450   455   460

act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt gtg   1443
Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe Val
                465   470   475

cag tgg ttg atg aat acc tgagaattct   1471
Gln Trp Leu Met Asn Thr
                480

<210> 3
<211> 4790
<212> DNA
<213> Artificial Sequence
<220>
<223> DNA sequence of artificial expression vector pCAGGS

<400> 3
gtcgacattg attattgact agttattaat agtaatcaat tacgggggtca ttagttcata   60

gcccatatat ggagttccgc gttacataac ttacggtaaa tggcccgcct ggctgaccgc   120

ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag   180

ggactttcca ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac   240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg   300

```
cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg    360

tattagtcat cgctattacc atgggtcgag gtgagcccca cgttctgctt cactctcccc    420

atctcccccc cctccccacc cccaattttg tatttattta tttttttaatt attttgtgca    480

gcgatggggg cggggggggg ggggcgcgc gccaggcggg gcggggcggg gcgaggggcg    540

gggcggggcg aggcggagag gtgcggcggc agccaatcag agcggcgcgc tccgaaagtt    600

tcctttttatg gcgaggcggc ggcggcggcg gccctataaa aagcgaagcg cgcggcgggc    660

gggagtcgct gcgttgcctt cgccccgtgc cccgctccgc gccgcctcgc gccgcccgcc    720

ccggctctga ctgaccgcgt tactcccaca ggtgagcggg cgggacggcc cttctcctcc    780

gggctgtaat tagcgcttgg tttaatgacg gctcgtttct tttctgtggc tgcgtgaaag    840

ccttaaaggg ctccgggagg gccctttgtg cggggggggag cggctcgggg ggtgcgtgcg    900

tgtgtgtgtg cgtggggagc gccgcgtgcg gcccgcgctg cccggcggct gtgagcgctg    960

cgggcgcggc gcggggcttt gtgcgctccg cgtgtgcgcg aggggagcgc ggccgggggc    1020

ggtgccccgc ggtgcggggg ggctgcgagg ggaacaaagg ctgcgtgcgg ggtgtgtgcg    1080

tggggggggtg agcaggggggt gtgggcgcgg cggtcgggct gtaacccccc cctgcacccc    1140

cctccccgag ttgctgagca cggcccggct tcgggtgcgg ggctccgtgc ggggcgtggc    1200

gcggggctcg ccgtgccggg cggggggtgg cggcaggtgg gggtgccggg cggggcgggg    1260

ccgcctcggg ccggggaggg ctcgggggag gggcgcggcg gccccggagc gccggcggct    1320

gtcgaggcgc ggcgagccgc agccattgcc ttttatggta atcgtgcgag agggcgcagg    1380
```

gacttccttt gtcccaaatc tggcggagcc gaaatctggg aggcgccgcc gcaccccctc 1440

tagcgggcgc gggcgaagcg gtgcggcgcc ggcaggaagg aaatgggcgg ggagggcctt 1500

cgtgcgtcgc cgcgccgccg tccccttctc catctccagc ctcggggctg ccgcaggggg 1560

acggctgcct tcgggggggga cggggcaggg cggggttcgg cttctggcgt gtgaccggcg 1620

gctctagagc ctctgctaac catgttcatg ccttcttctt tttcctacag ctcctgggca 1680

acgtgctggt tgttgtgctg tctcatcatt ttggcaaaga attcctcgag gaattcactc 1740

ctcaggtgca ggctgcctat cagaaggtgg tggctggtgt ggccaatgcc ctggctcaca 1800

aataccactg agatcttttt ccctctgcca aaaattatgg ggacatcatg aagccccttg 1860

agcatctgac ttctggctaa taaaggaaat ttattttcat tgcaatagtg tgttggaatt 1920

ttttgtgtct ctcactcgga aggacatatg ggagggcaaa tcatttaaaa catcagaatg 1980

agtatttggt ttagagtttg gcaacatatg ccatatgctg gctgccatga caaaggtgg 2040

ctataaagag gtcatcagta tatgaaacag ccccctgctg tccattcctt attccataga 2100

aaagccttga cttgaggtta gattttttttt atattttgtt ttgtgttatt tttttcttta 2160

acatccctaa aattttcctt acatgtttta ctagccagat ttttcctcct ctcctgacta 2220

ctcccagtca tagctgtccc tcttctctta tgaagatccc tcgacctgca gcccaagctt 2280

ggcgtaatca tggtcatagc tgtttcctgt gtgaaattgt tatccgctca caattccaca 2340

caacatacga gccggaagca taaagtgtaa agcctggggt gcctaatgag tgagctaact 2400

cacattaatt gcgttgcgct cactgcccgc tttccagtcg ggaaacctgt cgtgccagcg 2460

```
gatccgcatc tcaattagtc agcaaccata gtcccgcccc taactccgcc catcccgccc    2520

ctaactccgc ccagttccgc ccattctccg ccccatggct gactaatttt ttttatttat    2580

gcagaggccg aggccgcctc ggcctctgag ctattccaga agtagtgagg aggctttttt    2640

ggaggcctag gcttttgcaa aaagctaact tgtttattgc agcttataat ggttacaaat    2700

aaagcaatag catcacaaat ttcacaaata aagcattttt ttcactgcat tctagttgtg    2760

gtttgtccaa actcatcaat gtatcttatc atgtctggat ccgctgcatt aatgaatcgg    2820

ccaacgcgcg gggagaggcg gtttgcgtat tgggcgctct tccgcttcct cgctcactga    2880

ctcgctgcgc tcggtcgttc ggctgcggcg agcggtatca gctcactcaa aggcggtaat    2940

acggttatcc acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca    3000

aaaggccagg aaccgtaaaa aggccgcgtt gctggcgttt ttccataggc tccgcccccc    3060

tgacgagcat cacaaaaatc gacgctcaag tcagaggtgg cgaaacccga caggactata    3120

aagataccag gcgtttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc    3180

gcttaccgga tacctgtccg cctttctccc ttcgggaagc gtggcgcttt ctcaatgctc    3240

acgctgtagg tatctcagtt cggtgtaggt cgttcgctcc aagctgggct gtgtgcacga    3300

accccccgtt cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaaccc    3360

ggtaagacac gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag    3420

gtatgtaggc ggtgctacag agttcttgaa gtggtggcct aactacggct acactagaag    3480

gacagtattt ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag    3540
```

```
ctcttgatcc ggcaaacaaa ccaccgctgg tagcggtggt ttttttgttt gcaagcagca   3600

gattacgcgc agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga   3660

cgctcagtgg aacgaaaact cacgttaagg gattttggtc atgagattat caaaaaggat   3720

cttcacctag atcctttaa attaaaaatg aagttttaaa tcaatctaaa gtatatatga    3780

gtaaacttgg tctgacagtt accaatgctt aatcagtgag gcacctatct cagcgatctg   3840

tctatttcgt tcatccatag ttgcctgact ccccgtcgtg tagataacta cgatacggga   3900

gggcttacca tctggcccca gtgctgcaat gataccgcga gacccacgct caccggctcc   3960

agatttatca gcaataaacc agccagccgg aagggccgag cgcagaagtg gtcctgcaac   4020

tttatccgcc tccatccagt ctattaattg ttgccgggaa gctagagtaa gtagttcgcc   4080

agttaatagt ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cacgctcgtc   4140

gtttggtatg gcttcattca gctccggttc ccaacgatca aggcgagtta catgatcccc   4200

catgttgtgc aaaaaagcgg ttagctcctt cggtcctccg atcgttgtca gaagtaagtt   4260

ggccgcagtg ttatcactca tggttatggc agcactgcat aattctctta ctgtcatgcc   4320

atccgtaaga tgcttttctg tgactggtga gtactcaacc aagtcattct gagaatagtg   4380

tatgcggcga ccgagttgct cttgcccggc gtcaatacgg gataataccg cgccacatag   4440

cagaacttta aaagtgctca tcattggaaa acgttcttcg gggcgaaaac tctcaaggat   4500

cttaccgctg ttgagatcca gttcgatgta acccactcgt gcacccaact gatcttcagc   4560

atcttttact ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa   4620
```

aaagggaata agggcgacac ggaaatgttg aatactcata ctcttccttt ttcaatatta   4680

ttgaagcatt tatcagggtt attgtctcat gagcggatac atatttgaat gtatttagaa   4740

aaataaacaa ataggggttc cgcgcacatt tccccgaaaa gtgccacctg   4790

<210> 4
<211> 1233
<212> DNA
<213> Artificial Sequence
<220>
<221> CDS
<222> (13)..(1224)
<223> DNA insert encoding rat CTLA4, rat IgG Fc region and glucagon C19-29 region

<400> 4
gaattcattt aa atg gct tgt ctt gga ctc cag agg tac aaa act cac ctg   51
              Met Ala Cys Leu Gly Leu Gln Arg Tyr Lys Thr His Leu
               1   5   10

cag ctg cct tct agg act tgg cct ttt gga gtc ctg ctt tct ctt ctc   99
Gln Leu Pro Ser Arg Thr Trp Pro Phe Gly Val Leu Leu Ser Leu Leu
   15   20   25

ttc atc cca atc ttc tct gaa gcc ata caa gtg acc caa cct tca gtg   147
Phe Ile Pro Ile Phe Ser Glu Ala Ile Gln Val Thr Gln Pro Ser Val
30   35   40   45

gtg ttg gcc agc agc cac ggt gtc gcc agc ttt cca tgt gaa tat gca   195
Val Leu Ala Ser Ser His Gly Val Ala Ser Phe Pro Cys Glu Tyr Ala
                50   55   60

tct tca cac aac act gat gag gtc cgg gtg acg gtg ctg cgg cag aca   243
Ser Ser His Asn Thr Asp Glu Val Arg Val Thr Val Leu Arg Gln Thr

                    65   70   75

aat gac caa gtg aca gag gtc tgt gcc acg aca ttc aca gtg aag aac   291
Asn Asp Gln Val Thr Glu Val Cys Ala Thr Thr Phe Thr Val Lys Asn
        80   85   90

acg ttg ggc ttc cta gat gac ccc ttc tgc agt ggt acc ttt aat gaa   339
Thr Leu Gly Phe Leu Asp Asp Pro Phe Cys Ser Gly Thr Phe Asn Glu
        95   100   105

agc aga gtg aac ctc acc atc caa gga ctg agg gct gct gac acc gga   387
Ser Arg Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Ala Asp Thr Gly
110   115   120   125

ctg tac ttc tgc aag gtg gaa ctc atg tac cca ccg cca tac ttt gtg   435
Leu Tyr Phe Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Phe Val
                130   135   140

ggc atg ggc aac ggg acc cag att tat gtc atc gat cca gaa cca tgc   483
Gly Met Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys
                145   150   155

cca gat tca gac gcg gcc gcc gtg ccc aga aac tgt gga ggt gat tgc   531
Pro Asp Ser Asp Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp Cys
                160   165   170

aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc ttc   579
Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile Phe
        175   180   185

ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag gtc   627
Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
190   195   200   205

acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat ttc   675
Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His Phe

```
                  210                215                220

agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga cca      723
Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg Pro
            225                230                235

cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc ccc      771
Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
            240                245                250

atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag gtc      819
Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys Val
            255                260                265

acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa ccc      867
Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys Pro
270                275                280                285

gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc aag      915
Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr Lys
            290                295                300

gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa ggc      963
Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys Gly
            305                310                315

ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag cca     1011
Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln Pro
            320                325                330

cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg agt     1059
Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly Ser
        335                340                345

tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag cag     1107
Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln Gln
```

```
        350                 355                 360                 365

gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac cac      1155
Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
                370                 375                 380

cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat ttt      1203
His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp Phe
                385                 390                 395

gtg cag tgg ttg atg aat acc tgagaattc                                1233
Val Gln Trp Leu Met Asn Thr
            400
```

<210> 5
<211> 1143
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (13)..(1134)
<223> DNA insert encoding rat IL13, rat IgG Fc region and glucagon C19-29 region
<400> 5

```
gaattcattt aa atg gca ctc tgg gtg act gca gtc ctg gct ctc gct tgc      51
              Met Ala Leu Trp Val Thr Ala Val Leu Ala Leu Ala Cys
               1               5                   10

ctt ggt ggt ctt gcc acc cca ggg cca gtg cgg aga tcc aca tct ccc      99
Leu Gly Gly Leu Ala Thr Pro Gly Pro Val Arg Arg Ser Thr Ser Pro
    15                  20                  25

cct gtg gcc ctc agg gag ctt atc gag gag ctg agc aac atc aca caa     147
Pro Val Ala Leu Arg Glu Leu Ile Glu Glu Leu Ser Asn Ile Thr Gln
30                  35                  40                  45
```

```
gac cag aag act tcc ctg tgc aac agc agc atg gta tgg agc gtg gac        195
Asp Gln Lys Thr Ser Leu Cys Asn Ser Ser Met Val·Trp Ser Val Asp
                50              55              60

ctg aca gct ggc ggg ttc tgt gca gcc ctg gaa tcc ctg acc aac atc        243
Leu Thr Ala Gly Gly Phe Cys Ala Ala Leu Glu Ser Leu Thr Asn Ile
            65              70              75

tcc agt tgc aat gcc atc cac agg acc cag agg ata ttg aat ggc ctc        291
Ser Ser Cys Asn Ala Ile His Arg Thr Gln Arg Ile Leu Asn Gly Leu
            80              85              90

tgt aac caa aag gcc tcg gat gtg gct tcc agc ccc cca gat acc aaa        339
Cys Asn Gln Lys Ala Ser Asp Val Ala Ser Ser Pro Pro Asp Thr Lys
        95              100             105

atc gaa gta gcc cag ttt ata tca aaa ctg ctc aat tac tcc aag caa        387
Ile Glu Val Ala Gln Phe Ile Ser Lys Leu Leu Asn Tyr Ser Lys Gln
110             115             120             125

ctt ttc cgc tat ggc cac gcg gcc gcc gtg ccc aga aac tgt gga ggt        435
Leu Phe Arg Tyr Gly His Ala Ala Ala Val Pro Arg Asn Cys Gly Gly
                130             135             140

gat tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc        483
Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe
            145             150             155

atc ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct        531
Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro
            160             165             170

aag gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc        579
Lys Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val
        175             180             185
```

```
cat ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act        627
His Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr
190             195             200             205


cga cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa        675
Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu
            210             215             220


ctc ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc        723
Leu Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys
            225             230             235


aag gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc        771
Lys Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser
            240             245             250


aaa ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct        819
Lys Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro
    255             260             265


acc aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta        867
Thr Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val
270             275             280             285


aaa ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg        915
Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly
            290             295             300


cag cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat        963
Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp
            305             310             315


ggg agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg        1011
Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp
            320             325             330
```

```
cag cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac      1059
Gln Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His
    335             340             345


aac cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa      1107
Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln
350             355             360             365


gat ttt gtg cag tgg ttg atg aat acc tgagaattc                       1143
Asp Phe Val Gln Trp Leu Met Asn Thr
                370
```

<210> 6
<211> 825
<212> DNA
<213> Artificial Sequence
<220>
<221> CDS
<222> (13)..(816)
<223> DNA insert encoding rat signal peptide, rat IgG Fc region and glucagon C19-29
region

<400> 6

```
gaattcattt aa atg aag tcc tgc ggc ctg ttc cct ctc atg gtg ctc ctt      51
           Met Lys Ser Cys Gly Leu Phe Pro Leu Met Val Leu Leu
            1               5                   10


gct ctg ggt gta ctg gca ccc tgg agt gtg gaa gga gcg gcc gcc gtg      99
Ala Leu Gly Val Leu Ala Pro Trp Ser Val Glu Gly Ala Ala Ala Val
    15              20              25


ccc aga aac tgt gga ggt gat tgc aag cct tgt ata tgt aca ggc tca     147
Pro Arg Asn Cys Gly Gly Asp Cys Lys Pro Cys Ile Cys Thr Gly Ser
30              35              40              45
```

gaa gta tca tct gtc ttc atc ttc ccc cca aag ccc aaa gat gtg ctc   195
Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu
                50   55   60

acc atc act ctg act cct aag gtc acg tgt gtt gtg gta gac att agc   243
Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser
                65   70   75

cag gac gat ccc gag gtc cat ttc agc tgg ttt gta gat gac gtg gaa   291
Gln Asp Asp Pro Glu Val His Phe Ser Trp Phe Val Asp Asp Val Glu
                80   85   90

gtc cac aca gct cag act cga cca cca gag gag cag ttc aac agc act   339
Val His Thr Ala Gln Thr Arg Pro Pro Glu Glu Gln Phe Asn Ser Thr
     95   100   ·105

ttc cgc tca gtc agt gaa ctc ccc atc ctg cac cag gac tgg ctc aat   387
Phe Arg Ser Val Ser Glu Leu Pro Ile Leu His Gln Asp Trp Leu Asn
110   115   120   125

ggc agg acg ttc aga tgc aag gtc acc agt gca gct ttc cca tcc ccc   435
Gly Arg Thr Phe Arg Cys Lys Val Thr Ser Ala Ala Phe Pro Ser Pro
                130   135   140

atc gag aaa acc atc tcc aaa ccc gaa ggc aga aca caa gtt ccg cat   483
Ile Glu Lys Thr Ile Ser Lys Pro Glu Gly Arg Thr Gln Val Pro His
                145   150   155

gta tac acc atg tca cct acc aag gaa gag atg acc cag aat gaa gtc   531
Val Tyr Thr Met Ser Pro Thr Lys Glu Glu Met Thr Gln Asn Glu Val
                160   165   170

agt atc acc tgc atg gta aaa ggc ttc tat ccc cca gac att tat gtg   579
Ser Ile Thr Cys Met Val Lys Gly Phe Tyr Pro Pro Asp Ile Tyr Val
                175   180   185

```
gag tgg cag atg aac ggg cag cca cag gaa aac tac aag aac act cca        627
Glu Trp Gln Met Asn Gly Gln Pro Gln Glu Asn Tyr Lys Asn Thr Pro
190             195             200             205


cct acg atg gac aca gat ggg agt tac ttc ctc tac agc aag ctc aat        675
Pro Thr Met Asp Thr Asp Gly Ser Tyr Phe Leu Tyr Ser Lys Leu Asn
            210             215             220


gtg aag aag gaa aaa tgg cag cag gga aac acg ttc acg tgt tct gtg        723
Val Lys Lys Glu Lys Trp Gln Gln Gly Asn Thr Phe Thr Cys Ser Val
            225             230             235


ctg cat gaa ggc ctg cac aac cac cat act gag aag agt ctc tcc cac        771
Leu His Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His
            240             245             250


tct ccg ggt aaa gcc caa gat ttt gtg cag tgg ttg atg aat acc           816
Ser Pro Gly Lys Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
            255             260             265


tgagaattc                                                              825
```

<210> 7
<211> 1284
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (13)..(1275)
<223> DNA insert encoding rat IL1 receptor antagonist, rat IgG Fc region and glucagon C19-29 region

<400> 7
gaattcattt aa atg gaa atc tgc tgg gga ccc tac agt cac cta atc tct   51

```
            Met Glu Ile Cys Trp Gly Pro Tyr Ser His Leu Ile Ser
                 1               5                   10
```

```
ctc ctt ctc atc ctt ctg ttt cat tca gag gca gcc tgc cgc cct tct        99
Leu Leu Leu Ile Leu Leu Phe His Ser Glu Ala Ala Cys Arg Pro Ser
     15              20              25
```

```
ggg aaa aga ccc tgc aag atg caa gcc ttc aga atc tgg gat act aac       147
Gly Lys Arg Pro Cys Lys Met Gln Ala Phe Arg Ile Trp Asp Thr Asn
30              35              40              45
```

```
cag aag acc ttt tac ctg aga aac aac cag ctc att gct ggg tac tta       195
Gln Lys Thr Phe Tyr Leu Arg Asn Asn Gln Leu Ile Ala Gly Tyr Leu
                50              55              60
```

```
caa gga cca aat atc aaa cta gaa gaa aag ata gac atg gtg cct att       243
Gln Gly Pro Asn Ile Lys Leu Glu Glu Lys Ile Asp Met Val Pro Ile
                65              70              75
```

```
gac ctt cat agt gtg ttc ttg ggc atc cac ggg ggc aag ctg tgc ctg       291
Asp Leu His Ser Val Phe Leu Gly Ile His Gly Gly Lys Leu Cys Leu
            80              85              90
```

```
tct tgt gcc aag tct gga gat gat atc aag ctc cag ctg gag gaa gtt       339
Ser Cys Ala Lys Ser Gly Asp Asp Ile Lys Leu Gln Leu Glu Glu Val
    95              100             105
```

```
aac atc act gat ctg agc aag aac aaa gaa gaa gac aag cgc ttt acc       387
Asn Ile Thr Asp Leu Ser Lys Asn Lys Glu Glu Asp Lys Arg Phe Thr
110             115             120             125
```

```
ttc atc cgc tct gag aaa ggc ccc acc acc agc ttt gag tca gct gcc       435
Phe Ile Arg Ser Glu Lys Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala
                130             135             140
```

```
tgt cca gga tgg ttc ctc tgc aca aca cta gag gct gac cgt cct gtg       483
```

Cys Pro Gly Trp Phe Leu Cys Thr Thr Leu Glu Ala Asp Arg Pro Val
           145   150   155

agc ctc acc aac aca ccg gaa gag ccc ctt ata gtc acg aag ttc tac   531
Ser Leu Thr Asn Thr Pro Glu Glu Pro Leu Ile Val Thr Lys Phe Tyr
           160   165   170

ttc cag gaa gac caa gcg gcc gcc gtg ccc aga aac tgt gga ggt gat   579
Phe Gln Glu Asp Gln Ala Ala Ala Val Pro Arg Asn Cys Gly Gly Asp
        175   180   185

tgc aag cct tgt ata tgt aca ggc tca gaa gta tca tct gtc ttc atc   627
Cys Lys Pro Cys Ile Cys Thr Gly Ser Glu Val Ser Ser Val Phe Ile
190   195   200   205

ttc ccc cca aag ccc aaa gat gtg ctc acc atc act ctg act cct aag   675
Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                210   215   220

gtc acg tgt gtt gtg gta gac att agc cag gac gat ccc gag gtc cat   723
Val Thr Cys Val Val Val Asp Ile Ser Gln Asp Asp Pro Glu Val His
           225   230   235

ttc agc tgg ttt gta gat gac gtg gaa gtc cac aca gct cag act cga   771
Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Arg
           240   245   250

cca cca gag gag cag ttc aac agc act ttc cgc tca gtc agt gaa ctc   819
Pro Pro Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu
        255   260   265

ccc atc ctg cac cag gac tgg ctc aat ggc agg acg ttc aga tgc aag   867
Pro Ile Leu His Gln Asp Trp Leu Asn Gly Arg Thr Phe Arg Cys Lys
270   275   280   285

gtc acc agt gca gct ttc cca tcc ccc atc gag aaa acc atc tcc aaa   915

Val Thr Ser Ala Ala Phe Pro Ser Pro Ile Glu Lys Thr Ile Ser Lys
            290   295   300

ccc gaa ggc aga aca caa gtt ccg cat gta tac acc atg tca cct acc   963
Pro Glu Gly Arg Thr Gln Val Pro His Val Tyr Thr Met Ser Pro Thr
            305   310   315

aag gaa gag atg acc cag aat gaa gtc agt atc acc tgc atg gta aaa   1011
Lys Glu Glu Met Thr Gln Asn Glu Val Ser Ile Thr Cys Met Val Lys
            320   325   330

ggc ttc tat ccc cca gac att tat gtg gag tgg cag atg aac ggg cag   1059
Gly Phe Tyr Pro Pro Asp Ile Tyr Val Glu Trp Gln Met Asn Gly Gln
            335   340   345

cca cag gaa aac tac aag aac act cca cct acg atg gac aca gat ggg   1107
Pro Gln Glu Asn Tyr Lys Asn Thr Pro Pro Thr Met Asp Thr Asp Gly
350   355   360   365

agt tac ttc ctc tac agc aag ctc aat gtg aag aag gaa aaa tgg cag   1155
Ser Tyr Phe Leu Tyr Ser Lys Leu Asn Val Lys Lys Glu Lys Trp Gln
                370   375   380

cag gga aac acg ttc acg tgt tct gtg ctg cat gaa ggc ctg cac aac   1203
Gln Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
                385   390   395

cac cat act gag aag agt ctc tcc cac tct ccg ggt aaa gcc caa gat   1251
His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys Ala Gln Asp
            400   405   410

ttt gtg cag tgg ttg atg aat acc tgagaattc   1284
Phe Val Gln Trp Leu Met Asn Thr
            415   420

<210> 8
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (13)..(360)
<223> DNA insert encoding human IL8 and glucagon C19-29 region

<400> 8

```
gaattcattt aa atg act tcc aag ctg gcc gtg gct ctc ttg gca gcc ttc      51
               Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe
                1           5                   10


ctg att tct gca gct ctg tgt gaa ggt gca gtt ttg cca agg agt gct      99
Leu Ile Ser Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala
     15                  20                  25


aaa gaa ctt aga tgt cag tgc ata aag aca tac tcc aaa cct ttc cac     147
Lys Glu Leu Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His
30                  35                  40                  45


ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac tgc     195
Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys
                50                  55                  60


gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc tgt     243
Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys
                65                  70                  75


ctg gac ccc aag gaa aac tgg gtg cag agg gtt gtg gag aag ttt ttg     291
Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu
            80                  85                  90


aag agg gct gag aat tca gcg gcc gcc ccg ggt aaa gcc caa gat ttt     339
```

```
Lys Arg Ala Glu Asn Ser Ala Ala Ala Pro Gly Lys Ala Gln Asp Phe
    95                  100             105
```

```
gtg cag tgg ttg atg aat acc tgagaattc                           369
Val Gln Trp Leu Met Asn Thr
110             115
```

<210> 9
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 9
gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg   45

<210> 10
<211> 49
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 10
tcaaccactg cacaaaatct tgggctttac ccggagagtg ggagagact   49

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 11
gagaattcat ttaaatgaga gcggccgccg tgcccagaaa ctgtg   45

<210> 12
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IgG-glu19-29

<400> 12
gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc   50

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 13
gagaattcat ttaaatgatt ctgctggtgg tcctgatg   38

<210> 14
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IFN-rR-IgG-glu19-29

<400> 14

gcagcatcgc ggccgcttct tctctgtcat catggagaaa   40

<210> 15
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 15

gagaattcat ttaaatggct tgtcttggac tccagagg   38

<210> 16
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-CTLA4-IgG-glu19-29

<400> 16

gcagcatcgc ggccgcgtct gaatctgggc atggttctgg   40

<210> 17
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IL13-IgG-glu19-29

<400> 17

gagaattcat ttaaatggca ctctgggtga ctgcagtc   38

<210> 18
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IL13-IgG-glu19-29

<400> 18

gcagcatcgc ggccgcgtgg ccatagcgga aaagttgctt   40

<210> 19
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IL1RA-IgG-glu19-29

<400> 19

gagaattcat ttaaatggaa atctgctggg gaccctac   38

<210> 20
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223>   Oligonucleotide   primer   used   for   constructing   a   vector
pCAGGS-IL1RA-IgG-glu19-29

<400> 20

gcagcatcgc ggccgcttgg tcttcctgga agtagaactt   40

<210> 21
<211> 62
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 21

gagaattcat ttaaatgaga gcggccgccc cgggtaaagc ccaagatttt gtgcagtggt   60
tg   62

<210> 22
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-glu19-29

<400> 22

gagagagaga attctcaggt attcatcaac cactgcacaa aatcttgggc   50

<210> 23
<211> 38
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 23

gagaattcat ttaaatgact tccaagctgg ccgtggct   38

<210> 24
<211> 40
<212> DNA
<213> Artificial Sequence
<220>
<223> Oligonucleotide primer used for constructing a vector pCAGGS-IL8-glu19-29

<400> 24
gcagcatcgc ggccgctgaa ttctcagccc tcttcaaaaa   40